REVIEW

Insulin-like Growth Factors: Growth, Transgenes and Imprinting

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I BACKGROUND

The idea of integrating stable gene mutations into the germ line has long fascinated developmental biologists. Experimental gene modifications that influence subsequent developmental patterns have therefore been at the top of the list of priorities. The field of experimental embryology took off in the early 1960s when Krystof Tarkowski [86] and Beatrice Mintz [59] succeeded in fusing genetically distinct 8-cell embryos into stable chimaeras. In 1968 Richard Gardner [28] was able to show that by moving the inner cell mass from one embryo to another a chimaera could be formed. But it was not until 1974 when Jaenisch and Mintz [41] could report the first deliberate genetic modification of the mouse embryo. By infecting embryos at the blastocyst stage with SV40-virus they were able to demonstrate a stable integration of viral DNA in the live born progeny. This breakthrough was rapidly followed by Moloney murine leukemia virus mediated germ line transfer of foreign nucleic acid sequences [42]. Since that time the field has exploded, it appears pertinent to briefly discuss some key experimental landmarks during the last 20-year period.

It was in 1980 [30] that the pronuclear microinjection technique was devised and used to demonstrate the possibility of inserting foreign DNA from almost any source into the murine embryo. This technique can be applied to almost any animal species. The next important step forward was the demonstration that integrated foreign DNA can also be expressed. In 1981 Palmiter et al. [64] were able to ligate the 5' regulatory sequence of the murine metallothionein (MT1) gene with the core sequence of the herpes virus thymidine kinase gene. This transgene was injected into pronuclei and properly integrated. In the adult progeny, the herpes thymidine kinase gene was expressed in a pattern as expected from the MT1 gene with abundant expression in kidney and liver. Furthermore, it was concluded from this and subsequent studies that the actual integration site plays an inferior role in determining the level of expression. It is rather the cisacting regulatory sequences in and adjacent to genes that determine spatial and temporal transcription patterns [32, 63]. There are however important exceptions to this rule. In the case of the beta globin gene the absence of key enhancer elements makes it relatively more dependent on the integration site for adequate expression [13].

This implies that the interplay between structural regulatory elements is imperative in determining stage- and tissue-specific expression. If an isolated promoter sequence is fused with a heterologous coding region and integrated in the germ line, the expression pattern will in many cases differ from that of an integrated genomic clone containing the regulatory and structural elements in intact order. There are also transacting factors that affect expression of integrated foreign genes. The presence or absence of such transactivators indeed differ between species. When a human gene is integrated into transgenic mice, the transgene may therefore be expressed in organs that do normally not express the murine counterpart, but which are sites of expression in man.

Foreign genes normally integrate as head to tail concatamers into one unique site in the mouse genome. However at this single site a considerable number (from one to 50 copies) of transgenes can be integrated. There is ample evidence that this large scale integration is not always a straight forward process. It predisposes delays and recombinations leading to mosaic patterns. It can also lead to strange structural alterations of the mouse host genome including deletions, duplications, translocations and interspersion of islands of genomic DNA within the transgene sequences. The disruption of endogenous gene function upon transgene integration is also an alarmingly frequent event [58]

II METHODOLOGY

1. Pronuclear injection

Broadly, two approaches are currently employed in generating transgenic mice, leading to either over-expression or targeted alteration of the gene of interest. In the first approach, exogenous copies of the gene are incorporated into

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the genome with the aim of elevating its level of expression in vivo. This is usually achieved by injecting fertilised eggs, collected approximately 12 hr after mating has taken place, with linear cloned DNA fragments [39]. The injected embryos are then introduced into the uterus of receptive, pseudopregnant females, so that normal development can proceed. Liveborn mice are tested for the presence of the transgene by assaying biopsy material using DNA (Southern) blotting or polymerase chain reaction (PCR) techniques. Although the proportion of transgenic offspring which result is very much dependant on the nature of the injected DNA construct, frequencies of transgenesis over 20% can be achieved, representing one major advantage of this approach. This is offset against the principle disadvantage of this scheme, in that incorporation of the transgene into the genome occurs at essentially randomly determined positions. Since expression of the transgene can be influenced by sequences surrouding the integration site (so called position effects) and since transgene insertion can disrupt the function of a resident gene, the phenotype associated with any given DNA construct must be qualified by studying lines of transgenic mice representing at least two independent integration events.

2. Embryonic stem cells

In the second approach to producing transgenic mice, more recently developed technology allows the targeted alteration of specific endogenous genes by homologous recombination in embryonic stem (ES) cells. ES cells are derived from blastocyst embryos and can be maintained in culture for many generations before being microinjected into host blastocysts and returned to pseudopregnant females. Subsequently, they can colonise all tissues of the resulting animals, which develop to form chimeric mice. Chimeric animals in which the ES cells have given rise to germ cells can be bred to produce transgenic offspring which are entirely ES cell derived [40, 43]. Compared with the one cell embryos used for pronuclear microinjection, ES cells represent a more abundant source of starting material which can be manipulated in vitro over a much longer time period, greatly increasing the scope for the manipulation of the genome. This is essential to the success of the gene targeting scheme. Gene targeting requires a construct comprising sequences of the target gene, bearing a mutation which will alter or ablate its function, together with at least one selectable marker gene (such as neo', which confers resistance to the drug G418). Often the neo' gene is positioned within the construct such that it disrupts or replaces part of the coding region of the target gene. This construct can be introduced rapidly into many thousands of ES cells by electroporation. These cells are subsequently grown in the presence of G418 to identify resistant colonics which represent those cells in which the targeting construct was stably incorporated into the genome. The sequences of the target gene which flank the neo' gene provide regions of homology which allows recombination to take place such that the cloned DNA can replace the target gene following its introduction into embryonic stem cells. However, since homologous recombination events are usually much less frequent than random integration events, the G418 resistant ES cell colonies must be screened to establish which should be used to generate chimeras. This screening process is one of the rate limiting steps of this transgenic route since the homologous recombination events typically represent less than 0.1% of all stable transformants. However, this figure is constantly being improved with the development of methods to enrich for homologous recombination over random integration. These improvements include the use of a second selectable marker which must be lost from the targeting vector during homologous recombination to allow cell survival [53] and the use of DNA within the targeting construct which derives from the same mouse strain as the host ES cells [87, 88].

3. Strategies for increased expression

Perhaps the crudest overexpression strategy relies upon the use of an entire genomic sequence which contains the full coding sequence with cognate upstream regulatory elements as the transgene. This approach has had a practical advantage in compensating for defects in mutant animals lacking a specific gene. A classical experiment succeeded in restoring fertility in hypogonadal mice by introducing the gonadotropin releasing factor gene [55]. In addition to its simplicity, this method can be advantageous where it is important to reproduce the expression patterns of the gene of interest. For instance following cloning of the sex-determining gene Sry, its own regulatory sequences were relied upon to create transgenic mice which were XX males [46]. In this case accumulated molecular and genetic evidence indicated that the testis determining gene was normally expressed transiently in specific cells in the developing gonad [47].

A more widely appreciated approach is based upon the fusion of a coding sequence with a well characterized promoter sequence that operates in a multitude of tissues. Commonly used promoters that induce widespread expression are the actin, H2 and SV40 promoters. Other promoter sequences induce expression in a more limited spectrum of cells and tissues. The mouse Mammary Tumour Virus Long Terminal Repeat (MMTV-LTR) operates mainly in secretory epithelial cells, and as a result transgenes containing this promoter sequence are expressed specifically in this cell type. When the MMTV-LTR was fused with the Granulocyte Macrophage Colony Stimulating Factor gene a strange subset of phenotypes were observed amongst the offspring [48]. Other promoters that allow cell specific expression include the Immunoglobulin promoter. When this sequence was fused with the interleukin-6 (IL-6) gene, mice harbouring this transgene developed plasmocytosis, with IL-6 expressing B-cells circulating throughout the body giving rise to high circulating levels of IL-6 protein [82].

The options can be further narrowed by using tissue specific promoters. The first of its kind to be utilized for this purpose was the rat insulin promoter (RIP) which is only

active in pancreatic beta cells. By fusing RIP with a nerve growth factor (NGF) coding sequence a unique pattern of hyperinnervation of the islets of Langerhans was achieved [20]. The great advantage of this approach is that the phenotypic effects on a single organ is enabled. Now a plethora of organ specific promoters are used for the purpose of site directed expression of transgenes. The bovine keratin 10 promoter directs the expression of transgenes to the supra basal layer of the skin and to the forestomach [2]. Gene expression can be directed to the mammary gland by using either the Whey Acidic Protein (WAP) promoter [35] or the beta lactoglobulin promoter [91]. The latter promoter limits expression to the secretory epithelium of the mammary gland. Moreover, induction of beta lactoglobulin expression coincides with that of beta casein in the tissue, indicating that the pattern of expression is determined by the differentiated state of the mammary cells [35, 91]. Using this promoter, protein products of the transgene can be secreted into milk and form up to 10% of the total milk protein or 30% of whey protein [1]. To achieve kidney specific expression, much attention has been devoted to the three murine renin genes Ren-IC, Ren-1d and Ren-2. However, the three renin genes exhibit distinct expression profiles at a number of extra renal sites [27, 75, 76].

III TRANGENIC STUDIES INVOLVING INSULIN AND THE INSULIN-LIKE GROWTH FACTORS

Insulin and the insulin-like growth factors (IGF-I and IGF-II) are structurally related and share affinities for the same set of trans-membrane receptors (reviewed in [72]). Each factor exhibits a preference for the appropriately named receptor (insulin, IGF type 1 and IGF type 2) but can interact with the others. This family of growth factors and receptors represent probably the most intensively studied using mouse transgenesis; insulin, IGF-I and IGF-II have all been analysed using overexpression strategies and IGF-I, IGF-II and the IGF type 1 receptor have each been the subject of gene targeting experiments to disrupt their function in mice. These experiments have revealed much about the *in vivo* functions of these factors and collectively they amply demonstrate the effectiveness of applying transgenic techniques to the analysis of mammalian growth factors.

1. Insulin

In several reports a common strategy has been adopted to elevate insulin expression at the natural sites of synthesis [11, 26, 54, 74]. By introducing copies of the human insulin gene into mice it was possible to distinguish mRNA and protein of transgene and endogenous origin while harnessing the cognate promoter to ensure expression was obtained in the pancreatic islets. The efficacy of this approach is clear since in all cases transgene expression was restricted to the pancreas and in one case, by comparing various lengths of promoter sequence, it was established that as little as 168 bp upstream of the transcript initiation site are sufficient to

ensure correct tissue-specificity of expression from the insulin gene promoter [26]. In mice with detectable levels of human insulin, but no significant increase in total serum insulin levels, appropriate regulation of the human insulin transgene was established by challenging mice with glucose, amino acids or the hypoglycemic drug tolbutamide [11, 74]. In these cases normal pancreatic histology was reported and there were no obvious effects on growth. More recently it was shown that higher than normal serum insulin levels can result from similar transgenic experiments, consequently these mice are hyperglycemic in response to a glucose challenge and their normal fasting glucose levels suggest some insulin tolerance [54]. To date, however, transgenic experiments have not suggested any direct effects on growth in vivo, although insulin can promote growth in vitro [79] and is a routine addition in culture media. While it may be that insulin has no significant effect on growth in vivo further experiments, perhaps involving the targeted mutation of the insulin gene or its overexpression at ectopic sites and during earlier developmental stages, might be more revealing in this context.

2. IGF-I

A key role of IGF-I, in mediating the effects of growth hormone (GH) on postnatal growth, was proposed over ten years ago when adminstration of purified IGF-I was shown to stimulate growth in hypophysectomised rats [70]. This relationship was subsequently bome-out by experiments in which GH or IGF-I over-expression was achieved in transgenic mice. When rat or human GH genes were placed under the control of the mouse metallothionein I (mTM-I) gene promoter serum GH levels could be raised several hundred-fold, typically resulting in a 1.5-fold increase in adult body weight [64, 65]. Growth enhancement was detectable from about 3 weeks of age and was associated with elevated levels of circulating IGF-I. The rise in serum IGF-I was shown to preceed the acceleration in growth by about one week [56]. Although these data are consistent with the proposed role for IGF-I, the findings of Stewart et al. [80] suggest the increased circulating IGF-I might not be necessary to mediate GH action. These workers expressed human GH in mice using a mammary tumour virus LTR and these transgenic mice displayed supernormal growth kinetics similar to those described previously but did not always have high serum IGF-I levels. They suggest the extra growth results from direct GH action through the somatogenic and PRL receptors. Alternatively, stimulation of IGF-I production local to its sites of action might be the important factor as this could occur independently of changes in serum levels. In fact a combination fo direct and IGF-I mediated mechanisms of GH action remains likely and is consistent with the results of 1GF-I over-expression in transgenic mice [55]. Although only one of two lines of mice established using an mMT-1/ hIGF-I construct were found to express the introduced gene these mice were 1.3 fold larger than controls, which is within the range of the effect obtained with mMT-I/GH constructs. However, the phenotype of the IGF-I transgenic mice differed from that of GH trangenics, notably in the range of organs which were enlarged or exhibited histopathological changes, and that the onset of the effect on live weights was delayed until at least six weeks after birth [7, 16, 57, 66].

Mice lacking a functional IGF-I gene have recently been created by gene targeting [3, 52]. The homozygous mutants were approximately 60% normal size at birth and their survival into adulthood varied with genetic background. Postnatally, the surviving animals continued to grow slowly, eventually attaining only about 30% the weight of normal littermates. These experiments confirm unequivocally that IGF-I has a significant effect on growth during embryogenesis, before any effects of GH are manifest.

3. IGF-II

In contrast with studies involving IGF-I, attempts to produce mice over-expressing IGF-II using promoters with relatively broad fields of activity have been largely unsuccessful. At least three groups of researchers found that, at best, only low levels of transgene expression were obtained when using promoters from the mMT-I (expression reported in 2/ 17 transgenic lines (63)), rat IGF-II (0/4; (49)) and human H-2k (0/8; (21)) genes. In all of these cases no significant effects on growth were reported. This can be attributed to an embryonic lethal effect which is thought likely to result from the presence of excess IGF-II, perhaps at critical sites and/or periods during development. Recent genetic evidence supports this theory as mice lacking the type 2 IGF receptor (Thp mutant mice) usually die at mid-gestation, but this phenotype is rescued when they also lack a functional Igf-2 gene [25]. The principle role for the type 2 receptor seems to be one of targeting its ligands (IGF-II and mannose-6-phosphate) for lysosomal degradation, and not mitogenic signalling. Thus, the lethality observed in T^{hp} mice is seen as an absence of this important regulator of IGF-II action.

Very recently the problems associated with producing IGF-II transgenic mice were circumvented by using a keratin gene promoter which had previously provided tissue restricted expression of a *h-ras* transgene [2]. IGF-II transgene expression was seen in all of the transgenic lines established using this promotor (Ward *et al.*, unpublished). These mice exhibited dramatic local effects on growth, consistent both with the paracrine/autocrine mode of action suggested for IGF-II by *in situ* expression studies (reviewed in [90]) and with proposed roles for IGF-II in growth related diseases, including Beckwith-Wiedemann syndrome and certain cancers [51, 73, 89]. These over-expression experiments complement studies of mice in which the IGF-II gene was disrupted by gene targeting.

Growth of IGF-II null mice was compromised during development, but not postnatally as recorded for mice without an intact IGF-I gene, and their size at birth was about 60% that of their normal littermates. Further differences between IGF-I and IGF-II null mice demonstrated that IGF-II acts at least two embryonic days earlier than IGF-I and that only IGF-II has an effect on placental growth [3, 73, 89]. The type 1 receptor was also mutated as part of this spectacular series of experiments and IGF-I-R null mice were more severely dwarfed at birth than either of those lacking individual functioning IGF genes. The availability of these three types of gene targeted mice, together with Thp mutants, allowed the breeding of various double mutants [3, 25, 52]; some of their characteristics are summarized in Table 1. Comparison of all the resulting single and double mutants yeilded several important conclusions, including that IGF-I acts solely through the type 1 receptor (since the phenotypes of mice null for either Igf-1r or Igf-1 and Igf-1r were indistinguishable) while IGF-II acts through both the type 1 receptor and at least one other (since similar phenotypes were

TABLE 1. Gross effects on growth of mice null for IGF and/or IGF receptor functions

Nullitype	Birth weight (% normal)	Placenta	Onset	Notes
Igf-I	60%	100%	E13.5	Survival to adulthood varies with genetic background. Some distortion in prop- ortionality of features. De- lays in ossification.
Igf-2	60%	75%	E11	Proportionally dwarfed. De- lays in ossification.
IgfIr or Igf-1/IgfIr	45%	100%	E11	Neonatal death (respiratory failure). Marked hypoplasia in muscle and skin. Extended delays in ossification.
IgfIr/Igf-2 Igf-1/Igfr-2	30%	75%	E11	Neonatal death (respiratory failure). Marked hypoplasia in muscle and skin. Extended delays in ossification.
Igf2r			****	Mid-gestational lethality.
Igf-2/Igf2r	60%	75%	_	Neonatal lethality.

These results are implicit and all quantities are approximate. Data from (3, 14, 15, 25, 52). Note that Igf-2 results were obtained with heterozygous mutations, following paternal transmission of the null allele and the intact maternal allele is known to be expressed in some tissues.

displayed by mice null for either *Igf-1* and *Igf-2* or *Igf-1r* and *Igf-2* and in both cases these phenotypes were more severe than that of *Igf-1r* mutants). The identity of the second IGF-II receptor remains ambiguous, although it could be the insulin receptor, and this receptor was deemed the sole mediator of IGF-II action on placental growth.

IV TRANSCRIPTION FACTORS

One alternative approach to studying growth factor production in vivo, involves manipulation of relevant transcription factor genes and introducing them into transgenic animals. It has been suggested that many growth factor defects arise as a consequence of a defect in transcriptional regulation rather than mutations in the growth factor gene itself. This is particularly important in embryogenesis, and it was recently shown that deregulation of the pax-2 gene had a dramatic impact on kidney development [19]. This gene belongs to a family of transcription factors that display organ and stage specific activity. pax-2 is expressed in the embryonic kidney after mesenchymal induction, in the ureter epithelium and early epithelial structures [17]. Furthermore, its expression is repressed upon terminal differentiation but persists at increased levels in Wilms tumours [18]. In this respect it mirrors the transcriptional activity of the IGF II gene which makes studies of persistent pax-2 gene expression in transgenic animals particularly interesting. Deregulated pax-2 expression in transgenic mice gave rise to histologically abnormal and dysfunctional renal epithelium reminiscent of the congenital nephrotic syndrome. The interrelationship between pax-2 and IGF II and their combined detrimental impact on development however remains to be further clarified.

It has been shown that both the IGF-I and IGF-II gencs contain AP-1 binding sites [12, 45]. Therefore studies which aim at altering the availability of Fos and Jun proteins ought to influence the expression of the IGF genes and would be of particular interest from a developmental point of view. When both copies of *c-jun* were inactivated by homologous recombination, perfectly viable ES-cells were obtained [37]. When these were integrated into the germ line it was found that heterozygous mutant mice were normal, but embryos lacking c-jun, died at mid or late gestation, and displayed impaired hepatogenesis, altered fetal liver erythropoesis and generalized oedema. Moreover, it was found that c-jun -/-ES cells were capable of participation in development of all somatic cells in chimaeras except liver cells [38]. An example of the opposite approach, namely an overexpression of the AP-1 component fos yielded an unexpected series of results. Expression of c-fos has for more than a decade been considered an early step in the chain of events between growth stimulation and onset of DNA-synthesis. However, embryonic development is a fine balance between proliferation, differentiation and programmed cell death. By studying fos-lacZ transgenic mice it was possible to demonstrate that continuous fos expression begins hours or days before the morphological demise of a condemned cell. Expression, therefore appears to be a hall mark of terminal differentiation and a harbinger of death [77]. These examples show that alteration of transcription factors expression lead to dramatic biological effects in transgenic animals. Therefore they should be taken into account when growth factors are to be considered as prime candidates for developmental processes in transgenic animals.

V GROWTH FACTORS, TRANSGENESIS AND GENOMIC IMPRINTING

One surprising outcome of the IGF-II gene knock-out experiments was the finding that the growth deficient phenotype occurred in heterozygous mutant mice when the mutation was inherited from a male but not from a female [15]. This led to the discovery that IGF-II is subject to genomic imprinting, with only the allele inherited from the male being expressed in most tissues [14]. The phenomenon of genomic imprinting was known before this, since nuclear transplantation experiments had demonstrated the nonequivalence of the male and female genetic contribution in mammalian development [84, 85], but Igf-2 was the first gene known to be influenced by this peculiar form of regulation. Soon afterwards the Igf-2r gene was also shown to be imprinted after it was mapped within deletions of chromosome 17 harboured by the Thp and Tlub2 mutants [4]. In this case, in accord with the lethality associated with female but not male transmission of the Thp and Tlub2 mutations, the maternal allele was found to be active.

Opposite imprinting of the Igf-2 and Igf-2r genes immediately brought to life an hypothesis of parent-offspring conflict predicted in plant and animal species in which the growth of progeny is dependent on a maternal nutient supply (e.g. the mammalian placenta) and in which multiple paternity is likely among offspring of individual females [45]. Under these circumstances, and given that larger offspring are the most well equipped to survive, the interest of the father is best served if each of his progeny are as large and strong as possible. As there is a chance that he may be usurped the father makes the most of each opportunity to reproduce although this might involve an increased burden on the mother. Obviously, she is guaranteed to be equally related to each of her offspring, irrespective of any changes in mate choice and it follows that it is in the mothers interest to distribute resources evenly among her unborn young whether within a litter or in conserving the capacity to produce later litters. Since this parental conflict of interest requires that a "choice" is made regarding growth during embryonic life, Haig and Westoby [34] suggested that this would be reflected at the molecular level. That Igf-2 and the Igf-2r can be viewed as molecular weapons in this conflict is entirely in keeping with their antagonistic effects on growth and, of course, that it is respectively the paternally- and maternallyderived copies of each that are expressed [33].

Genomic imprinting of human IGF-II was recently con-

firmed [29] and is implicated in the ontogeny of the fetal overgrowth disease Beckwith Wiedemann syndrome [36]. Furthermore, it has been suggested that mis-regulation of imprinted genes might be important in a range of neoplastic diseases since, for instance, as only one allele is normally expressed then a single mutation would effectively result in a nullisomy. Conversely, activation of the normally silent allele would result in the gene product being overrepresented [23, 44]. Indeed relaxation of imprinting was recently demonstrated for IGF-II in a proportion of Wilms' tumours [60, 67].

There is one further intriguing link between IGF-II and imprinting in that the H19 gene, located only about 80 kb from IGF-II [92], is also imprinted with the maternally derived copy being active in mouse and man [6, 93]. This gene has no ascribed function in vivo and might exert its effect as an RNA product since it does not encode an open reading frame [8]. However, the influence of H19 on development is evidenced by transgenic experiments in which overexpression of intact H19 genes resulted in midgestational lethality [10]. It has been suggested that the regulation of IGF-II and H19 might be linked in some fashion since these two oppositely imprinted genes are such near neighbours [5, 83, 92]. The perceived importance of genomic imprinting in both normal development and growth related disease has fuelled an intense interest in achieving an understanding of the mechanism which underlies this phenomenon. An epigenetic signal which can be appropriately modified during passage of genes through either the male or female germline is required to establish and maintain allele specific expression of imprinted genes. Studies of the Igf-2 [69], Igf-2r [81] and H19 [5, 24] genes indicate that DNA methylation might be involved in this process, and this was recently confirmed through the discovery that all three loci were lost in mice with a methyltransferase gene deficiency [50]. However, the race towards a full understanding is far from over. Early evidence suggests that not all of the signals required for properly imprinted expression have yet been discovered as only a minor proportion of *Igf-2* [49] and *H19* [5] transgenes behave in accord with their parent of origin, but it is without doubt that transgenesis will play a key role in unravelling this biological conundrum.

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